

1033592-000005
SEQUENCE LISTING

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LON-NROTH, IVAR
ERIKSSON, PETER
PERSSON, ANDERS

<120> NOVEL USE OF ANTISECRETORY FACTOR

<130> 1003301-000258

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<150> PCT/SE04/001369

<151> 2004-09-24

<150> GB 0322645.3

<151> 2003-09-26

<160> 6

<170> PatentIn Ver. 3.3

<210> 1
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<212> PRT
<213> Homo sapiens

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Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
20 25 30
Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn
35 40 45
Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
50 55 60
Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
65 70 75 80
Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
85 90 95
Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
100 105 110
Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
115 120 125
Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
130 135 140
Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145 150 155 160
Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
165 170 175
Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
180 185 190

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Gly	Gly	Ala	Met	Leu	Gly	Leu	Gly	Ala	Ser	Asp	Phe	Glu	Phe	Gly	Val
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Asp	Pro	Ser	Ala	Asp	Pro	Glu	Leu	Ala	Leu	Ala	Leu	Arg	Val	Ser	Met
210					215						220				
Glu	Glu	Gln	Arg	His	Ala	Gly	Gly	Ala	Arg	Arg	Ala	Ala	Arg	Ala	
225					230				235						240
Ser	Ala	Ala	Glu	Ala	Gly	Ile	Ala	Thr	Thr	Gly	Thr	Glu	Asp	Ser	Asp
			245					250					255		
Asp	Ala	Leu	Leu	Lys	Met	Thr	Ile	Ser	Gln	Gln	Glu	Phe	Gly	Arg	Thr
					260			265				270			
Gly	Leu	Pro	Asp	Leu	Ser	Ser	Ser	Thr	Glu	Glu	Glu	Glu	Ile	Ala	Tyr
					275			280				285			
Ala	Met	Gln	Met	Ser	Leu	Gln	Gly	Ala	Glu	Phe	Gly	Gln	Ala	Glu	Ser
					290			295				300			
Ala	Asp	Ile	Asp	Ala	Ser	Ser	Ala	Met	Asp	Thr	Ser	Glu	Pro	Ala	Lys
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Glu	Glu	Asp	Asp	Tyr	Asp	Val	Met	Gln	Asp	Pro	Glu	Phe	Leu	Gln	Ser
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Val	Leu	Glu	Asn	Leu	Pro	Gly	Val	Asp	Pro	Asn	Asn	Glu	Ala	Ile	Arg
					340			345					350		
Asn	Ala	Met	Gly	Ser	Leu	Pro	Pro	Arg	Pro	Pro	Arg	Thr	Ala	Arg	Arg
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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr
1 5 10 15
atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat 155
Met Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp
20 25 30
gct gtc aac ata gtt tgt cat tca aag acc cgc agc aac cct gag aac 203
Ala Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn
35 40 45
aac gtg ggc ctt atc aca ctg gct aat gac tgt gaa gtg ctg acc aca 251
Asn Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr
50 55 60
ctc acc cca gac act ggc cgt atc ctg tcc aag cta cat act gtc caa 299
Leu Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln
65 70 75

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ccc aag ggc aag atc acc ttc tgc acg ggc atc cgc gtg gcc cat ctg Pro Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu 80 85 90 95	347
gct ctg aag cac cga caa ggc aag aat cac aag atg cgc atc att gcc Ala Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala 100 105 110	395
ttt gtg gga agc cca gtg gag gac aat gag aag gat ctg gtg aaa ctg Phe Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu 115 120 125	443
gct aaa cgc ctc aag aag gag aaa gta aat gtt gac att atc aat ttt Ala Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe 130 135 140	491
ggg gaa gag gag gtg aac aca gaa aag ctg aca gcc ttt gta aac acg Gly Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr 145 150 155	539
ttg aat ggc aaa gat gga acc ggt tct cat ctg gtg aca gtg cct cct Leu Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro 160 165 170 175	587
ggg ccc agt ttg gct gat gct ctc atc agt tct ccg att ttg gct ggt Gly Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly 180 185 190	635
gaa ggt ggt gcc atg ctg ggt ctt ggt gcc agt gac ttt gaa ttt gga Glu Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly 195 200 205	683
gta gat ccc agt gct gat cct gag ctg gcc ttg gcc ctt cgt gta tct Val Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser 210 215 220	731
atg gaa gag cag cgg cac gca gga gga gga gcg cgg cgg gca gct cga Met Glu Glu Gln Arg His Ala Gly Gly Ala Arg Arg Ala Ala Arg 225 230 235	779
gct tct gct gct gag gcc ggg att gct acg act ggg act gaa gac tca Ala Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser 240 245 250 255	827
gac gat gcc ctg ctg aag atg acc atc agc cag caa gag ttt ggc cgc Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg 260 265 270	875
act ggg ctt cct gac cta agc agt agt act gag gaa gag gag att gct Thr Gly Leu Pro Asp Leu Ser Ser Thr Glu Glu Glu Glu Ile Ala 275 280 285	923
tat gcc atg cag atg tcc ctg cag gga gca gag ttt ggc cag gcg gaa Tyr Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu 290 295 300	971
tca gca gac att gat gcc agc tca gct atg gac aca tct gag cca gcc Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala 305 310 315	1019
aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln 320 325 330 335	1067
agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile 340 345 350	1115

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cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga 1163
Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg
355 360 365

agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg 1208
Arg Thr Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
370 375 380

tagctgagtc tgcttaggg actggaaagc acgaaataa gggtagatg tggtatctg 1268
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amino acid sequence

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
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35 40 45

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Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
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Val Gly Leu
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25

30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn

35

40

45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met

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Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala

20

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30

Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn

35

40

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Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu

50

55

60

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Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
65 70 75 80

Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
85 90 95

Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
100 105 110

Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
115 120 125

Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
130 135 140

Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145 150 155 160

Asn Gly Lys